



SEQUENCE LISTING

<110> Chan, Lia Raquel  
Gonzalez, Daniel H.  
Dezar, Carlos A.  
Gago, Gabriela Marisa  
Dunan, Claudio Marcelo

<120> Transcription Factor Gene Induced by Water Deficit Conditions and  
Absciscic Acid from Helianthus Annuus, Promoter and Transgenic Plants

<130> 2510.0040000/JAG/SAC

<140> 10/520,333

<141> 2003-05-02

<150> PCT/US2003/013770

<151> 2003-05-02

<160> 30

<170> PatentIn version 3.1

<210> 1

<211> 774

<212> DNA

<213> Helianthus annuus

<400> 1

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aaacgattta ccgacaaaca aataagtttc ctagagtaca tgtttgagac acagtcgaga	180
cccgagttaa ggatgaaaca ccagttggca cataaactcg ggcttcatcc tcgtcaagtg	240
gcgatatggt tccagaacaa acgcgcgcga tcaaagtcga ggcagattga gcaagagtat	300
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agttggaggt gctgagaaat gtagcagaaa agcatcaaga gaaaactagt agtagtggca	540
gcggtgaaga atcggtgat cggtttacga actctccgga cgttatgttt ggtcaagaaa	600
tgaatgttcc gttttgcgac ggttttgcgt actttgaaga aggaaacagt ttgttggaga	660
ttgaagaaca actgccagac cctcaaaagt ggtgggagtt ctaaagagta aagaaggatg	720
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<210> 2  
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 <213> Helianthus annuus

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 aaacgattta ccgacaaaca aataagtttc ctagagtaca tggttgagac acagtcgaga 180  
 cccgagttta ggatgaaaca ccagttggca cataaactcg ggcttcatcc tcgtcaagtg 240  
 gcgatatggg tccagaacaa acgcgcgcga tcaaagtcga ggcagattga gcaagagtat 300  
 aacgcgctaa agcataacta cgagacgctt gcgtctaaat ccgagtcctt aaagaaagag 360  
 aatcaggccc tactcaatca gttggagggt ctgagaaatg tagcagaaaa gcatcaagag 420  
 aaaactagta gtagtggcag cggatgaaga tcggatgatc gggttacgaa ctctccggac 480  
 gttatgtttg gtcaagaaat gaatgttccg ttttgcgacg gttttgcgta ctttgaagaa 540  
 ggaaacagtt tggtggagat tgaagaacaa ctgccagacc ctcaaaagtg gtgggagttc 600  
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 gtttacactt tgt 673

<210> 3  
 <211> 1221  
 <212> DNA  
 <213> Helianthus annuus

<220>  
 <221> promoter  
 <222> (1)..(1221)  
 <223> Large allele

<400> 3  
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 atattaaaag tagtagcccc cccccccatt tggtacctac catttccac ttttaataatc 180  
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 ccaaattttt tttagtggaa acaaatcc ccaaatagaa tactaacgaa attcatcgca 300  
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aaaaccgcgt tggctcaagg atcgaactag cgattgctgc ctactcgctt aatctcccat	720
catcaacagg tgccgccgaa acaaaatgct gggggcgggg gttgaacctt ggtccagtga	780
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cttaacctaa gtccgccttt gtctggatca cgtgaaacat caggctcttc ccttaccagt	960
ccagctacga ctcatgaca aaatatcaaa accatatgat tttgagtttt atctcaaccg	1020
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tgcgttgaaa aggacaaaac aggtaggatt cttgtcaaat tcaacgcgta cacctgtgct	1140
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<210> 4  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide based on the promoter and having Hind I  
 II site

<400> 4	
gcgaagcttg atgcgaacga gtggttta	28

<210> 5  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide based on the promoter and having Sal I  
 site

<400> 5	
gcggtcgaca cctggcacat cgtatctt	28

<210> 6  
 <211> 27

<212> DNA  
 <213> Artificial Sequence  
  
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 <223> Designed oligonucleotide based on the promoter and having Bam HI site  
  
 <400> 6  
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 <210> 7  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <400> 7  
 cccaagctta acctaagtcc gcctttg 27  
  
 <210> 8  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Designed oligonucleotide based on the promoter and having Hind II I site  
  
 <400> 8  
 ggcaagctta tctcaaccga aagtgac 27  
  
 <210> 9  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Designed oligonucleotide based on the 5' promoter  
  
 <400> 9  
 atttcgcaag tagtccatt 19  
  
 <210> 10  
 <211> 1015  
 <212> DNA  
 <213> Helianthus annuus  
  
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ccaaatTTTT tttaatggaa aacaaatact tcaaatgcac tattgggtgaa attcaccaca 300
tcagaatata cccgtctcta ctcatctact ggccaacgaa tcttcacggg ggaaaccctc 360
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cataaccaa acgtgtaa acgtgtaa acgtgtaa ccattgcgtt gaaaaggaca aaacaggtag 900
gattcttgtc aaattcaacg cgtacacctg tgcttcatct aaaccata ctttaagaac 960
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<210> 11
<211> 28
<212> DNA
<213> Artificial Sequence

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<220>
<223> Designed oligonucleotide that matches nucleotides 81-100 of the H
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<400> 11
ggcggatcca acagaaacaa ccaccagg 28

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<210> 12
<211> 29
<212> DNA
<213> Artificial Sequence

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<220>
<223> Designed oligonucleotide for cloning 5' cDNA and having Bam HI s
ite

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<400> 12
ggcggatccc ctggtggttg tttctgttg 29

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<210> 13  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> oligonucleotide based on 5' cDNA and having Xho I site  
  
 <400> 13  
 gaggactcga gctcaagttt tttttttttt tttt 34  
  
 <210> 14  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide based on 5' cDNA and having Xho I site  
  
 <400> 14  
 gaggactcga gctcaagc 18  
  
 <210> 15  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Designed oligonucleotide based on the promoter and having Eco RI  
 site  
  
 <400> 15  
 gccgaattca gattgagcaa gagtataac 29  
  
 <210> 16  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Designed oligonucleotide based on the promoter  
  
 <400> 16  
 acctttataa agaccactc 19  
  
 <210> 17  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Designed oligonucleotide based on the promoter

<400> 17  
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<210> 18  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide to DNA-binding assays

<400> 18  
 aattcagatc tcaataattg agag 24

<210> 19  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide to DNA-binding assays

<400> 19  
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<210> 20  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide having Bam HI site

<400> 20  
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<210> 21  
 <211> 30  
 <212> DNA  
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<220>  
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<400> 21  
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<210> 22  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Oligonucleotide having Bam HI site

<400> 22  
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27

7

<210> 23  
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<212> DNA  
<213> Helianthus annuus

<220>  
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<222> (5)..(5)  
<223> n is a or t

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9

<210> 24  
<211> 181  
<212> PRT  
<213> Helianthus annuus

<400> 24

Met Ser Leu Gln Gln Val Pro Thr Thr Glu Thr Thr Thr Arg Lys Asn  
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Arg Asn Glu Gly Arg Lys Arg Phe Thr Asp Lys Gln Ile Ser Phe Leu  
20 25 30

Glu Tyr Met Phe Glu Thr Gln Ser Arg Pro Glu Leu Arg Met Lys His  
35 40 45

Gln Leu Ala His Lys Leu Gly Leu His Pro Arg Gln Val Ala Ile Trp  
50 55 60

Phe Gln Asn Lys Arg Ala Arg Ser Lys Ser Arg Gln Ile Glu Gln Glu  
65 70 75 80

Tyr Asn Ala Leu Lys His Asn Tyr Glu Thr Leu Ala Ser Lys Ser Glu  
85 90 95

Ser Leu Lys Lys Glu Asn Gln Ala Leu Leu Asn Gln Leu Glu Val Leu



100	105	110
Arg Asn Val Ala Glu Lys His Gln Glu Lys Thr Ser Ser Ser Gly Ser		
115	120	125
Gly Glu Glu Ser Asp Asp Arg Phe Thr Asn Ser Pro Asp Val Met Phe		
130	135	140
Gly Gln Glu Met Asn Val Pro Phe Cys Asp Gly Phe Ala Tyr Phe Glu		
145	150	155
Glu Gly Asn Ser Leu Leu Glu Ile Glu Glu Gln Leu Pro Asp Pro Gln		
	165	170
Lys Trp Trp Glu Phe		
180		
<210> 25		
<211> 99		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> Synthetic Hd-Zip domain of Athb-1		
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Glu Lys Ser Phe Glu Thr Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr		
20	25	30
Gln Leu Ala Lys Lys Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp		
35	40	45
Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Arg Asp		
50	55	60
Tyr Asp Leu Leu Lys Ser Thr Tyr Asp Gln Leu Leu Ser Asn Tyr Asp		
65	70	75
Ser Ile Val Met Asp Asn Asp Lys Leu Arg Ser Glu Val Thr Ser Leu		
85	90	95

Thr Glu Lys

<210> 26  
<211> 99  
<212> PRT  
<213> Artificial Sequence

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<223> Synthetic Hd-Zip domain of Athb-6

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Leu Ser Glu Lys Lys Arg Arg Leu Ser Ile Asn Gln Val Lys Ala Leu  
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Glu Lys Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Val  
20 25 30

Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp  
35 40 45

Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp  
50 55 60

Tyr Gly Val Leu Lys Thr Gln Tyr Asp Ser Leu Arg His Asn Phe Asp  
65 70 75 80

Ser Leu Arg Arg Asp Asn Glu Ser Leu Leu Gln Glu Ile Ser Lys Leu  
85 90 95

Lys Thr Lys

<210> 27  
<211> 99  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Hd-Zip domain of Athb-7

<400> 27

Asn Lys Asn Asn Gln Arg Arg Phe Ser Asp Glu Gln Ile Lys Ser Leu  
1 5 10 15

Glu Met Met Phe Glu Ser Glu Thr Arg Leu Glu Pro Arg Lys Lys Val

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Gln	Leu	Ala	Arg	Glu	Leu	Gly
	35				40	
Leu	Gln	Pro	Arg	Gln	Val	Ala
					45	
Ile	Trp					
Phe	Gln	Asn	Lys	Arg	Ala	Arg
	50				55	
Trp	Lys	Ser	Lys	Gln	Leu	Glu
				60		
Thr	Glu					
Tyr	Asn	Ile	Leu	Arg	Gln	Asn
	65			70		
Tyr	Asp	Asn	Leu	Ala	Ser	Gln
			75			
Phe	Glu					
						80
Ser	Leu	Lys	Lys	Glu	Lys	Gln
				85		
Ala	Leu	Val	Ser	Glu	Leu	Gln
		90				
Arg	Leu					
						95

Lys Glu Ala

<210> 28  
 <211> 99  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Hd-Zip domain of Athb-12

<400> 28

Lys	Ser	Asn	Asn	Gln	Lys	Arg	Phe	Asn	Glu	Glu	Gln	Ile	Lys	Ser	Leu
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			20					25					30		
Gln	Val	Ala	Arg	Glu	Leu	Gly	Leu	Gln	Pro	Arg	Gln	Met	Thr	Ile	Trp
		35					40					45			
Phe	Gln	Asn	Lys	Arg	Ala	Arg	Trp	Lys	Thr	Lys	Gln	Leu	Glu	Lys	Glu
	50					55					60				
Tyr	Asn	Thr	Leu	Arg	Ala	Asn	Tyr	Asn	Asn	Leu	Ala	Ser	Gln	Phe	Glu
	65				70				75					80	
Ile	Met	Lys	Lys	Glu	Lys	Gln	Ser	Leu	Val	Ser	Glu	Leu	Gln	Arg	Leu
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Asn Glu Glu

<210> 29  
<211> 99  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Hd-Zip domain of Hahb-4

<400> 29

Arg Asn Glu Gly Arg Lys Arg Phe Thr Asp Lys Gln Ile Ser Phe Leu  
1 5 10 15

Glu Tyr Met Phe Glu Thr Gln Ser Arg Pro Glu Leu Arg Met Lys His  
20 25 30

Gln Leu Ala His Lys Leu Gly Leu His Pro Arg Gln Val Ala Ile Trp  
35 40 45

Phe Gln Asn Lys Arg Ala Arg Ser Lys Ser Arg Gln Ile Glu Gln Glu  
50 55 60

Tyr Asn Ala Leu Lys His Asn Tyr Glu Thr Leu Ala Ser Lys Ser Glu  
65 70 75 80

Ser Leu Lys Lys Glu Asn Gln Ala Leu Leu Asn Gln Leu Glu Val Leu  
85 90 95

Arg Asn Val

<210> 30  
<211> 66  
<212> PRT  
<213> Artificial Sequence

<220> 30  
<223> Synthetic fragment of Hahb-4

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1 5 10 15

Ser Asp Asp Arg Phe Thr Asn Ser Pro Asp Val Met Phe Gly Gln Glu  
20 25 30

Met Asn Val Pro Phe Cys Asp Gly Phe Ala Tyr Phe Glu Glu Gly Asn  
35 40 45

Ser Leu Leu Glu Ile Glu Glu Gln Leu Pro Asp Pro Gln Lys Trp Trp  
50 55 60

Glu Phe  
65